

*Wasted*

# **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/367,013

Art Unit / Team No. : 1652

Date Processed by STIC: 5/5/2000

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/367,013DATE: 05/05/2000  
TIME: 11:03:38

INPUT SET: S35428.raw

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: KNUTZON, DEBORAH  
MURKERJI, PRADIP  
HUANG, YUNG-SHENG  
THURMOND, JENNIFER  
CHAUDHARY, SUNITA  
LEONARD, AMANDA

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

(iii) NUMBER OF SEQUENCES: 40

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LIMBACH AND LIMBACH LLP  
(B) STREET: 2001 FERRY BUILDING  
(C) CITY: SAN FRANCISCO  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94111

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Microsoft Word

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) ~~FILE~~ FILING DATE:

(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: WARD, MICHAEL R.  
(B) REGISTRATION NUMBER: 38,651  
(C) REFERENCE/DOCKET NUMBER: CGAB-210

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 433-4150  
(B) TELEFAX: (415) 433-8716  
(C) TELEX: N/A

Does Not Comply  
Corrected Diskette Needed  
*Errors throughout*

--&gt;

INPUT SET: S35428.raw

46

## ERRORED SEQUENCES FOLLOW:

857 (2) INFORMATION FOR SEQ ID NO:20:

858

859 (i) SEQUENCE CHARACTERISTICS:

860 (A) LENGTH: 227 amino acids

861 (B) TYPE: amino acid

862 (C) STRANDEDNESS: Not Relevant

863 (D) TOPOLOGY: linear

864

865 (ii) MOLECULE TYPE: peptide

866

867 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

868

869 Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln

870 1 5 10 15

871 His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr

872 20 25 30

873 Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly

874 35 40 45

875 Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr

876 50 55 60

877 Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro

878 65 70 75

879 Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile

880 80 85 90

881 Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val

882 95 100 105

883 Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg

884 110 115 120

885 Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln

886 125 130 135

887 Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr

888 140 145 150

889 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe

890 155 160 165

891 Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val

892 170 175 180

893 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro

894 185 190 195

895 Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys

896 200 205 210

897 Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys

898 215 220 225

899 Asp Asp Xaa

900

901

927 (2) INFORMATION FOR SEQ ID NO:22:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:39

INPUT SET: S35428.raw

928  
929 (i) SEQUENCE CHARACTERISTICS:  
--> 930 (A) LENGTH: 87 amino acids 102 shown  
931 (B) TYPE: amino acid  
932 (C) STRANDEDNESS: Not Relevant  
933 (D) TOPOLOGY: linear  
934  
935 (ii) MOLECULE TYPE: peptide  
936  
937 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
938  
939 Phe Trp Lys Xaa Pro Ser Xaa Pro Arg Xaa Xaa Gln Val Xaa Gly  
940 1 5 10 15  
941 Ala Glu Xaa Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys  
942 20 25 30  
943 Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu  
944 35 40 45  
945 Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe  
946 50 55 60  
947 Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp  
948 65 70 75  
949 Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu  
950 80 85 90  
951 Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
952 85 95  
953 100  
954  
955  
956  
957  
958

959 (2) INFORMATION FOR SEQ ID NO:23:  
960  
961 (i) SEQUENCE CHARACTERISTICS:  
--> 962 (A) LENGTH: 520 nucleic acids  
963 (B) TYPE: amino acid nucleic acid  
964 (C) STRANDEDNESS: Not Relevant  
965 (D) TOPOLOGY: linear  
966  
967 (ii) MOLECULE TYPE: nucleic acid  
968  
969 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
970  
971

972 GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG 60  
973 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC 120  
974 ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180  
975 GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240  
976 GGTTCGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCCA 300  
977 CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360  
978 ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420  
979 TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480

This should be  
Boxes below are in bold  
print due to above error.

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/367,013DATE: 05/05/2000  
TIME: 11:03:39

INPUT SET: S35428.raw

--> 980 TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTCCCGC  
981  
982

520

1043 (2) INFORMATION FOR SEQ ID NO:26:  
1044  
1045 (i) SEQUENCE CHARACTERISTICS:  
--> 1046 (A) LENGTH: 125 amino acids 140 shown  
1047 (B) TYPE: amino acid  
1048 (C) STRANDEDNESS: Not Relevant  
1049 (D) TOPOLOGY: linear  
1050  
1051 (ii) MOLECULE TYPE: peptide  
1052  
1053 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:  
1054  
1055  
1056 Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly  
1057 1 5 10 15  
1058 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu  
1059 20 25 30  
1060 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser  
1061 35 40 45  
1062 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser  
1063 50 55 60  
1064 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser  
1065 65 70 75  
1066 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe  
1067 65 80 70 85 75 90  
1068 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln  
1069 80 85 90  
1070 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val  
1071 95 100 105  
1072 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val  
1073 110 115 120  
1074 Arg Lys Val Arg Pro  
1075 125  
1076

1478 (2) INFORMATION FOR SEQ ID NO:34:  
1479  
1480 (i) SEQUENCE CHARACTERISTICS:  
--> 1481 (A) LENGTH: 411 amino acids 406 shown  
1482 (B) TYPE: amino acid  
1483 (C) STRANDEDNESS: single  
1484 (D) TOPOLOGY: linear  
1485  
1486 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)  
1487  
1488 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:  
1489  
1490  
1491 His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:39

INPUT SET: S35428.raw

1492	1	5	10	15
1493	Lys Ser Leu Met	Lys Pro Asp Pro Asn	Leu Ile Trp Ile Ile	Ile
1494		20	25	30
1495	Met Met Val Leu	Thr Gln Leu Gly Ala	Phe Tyr Ile Val Lys	Asp
1496		35	40	45
1497	Leu Asp Trp Lys	Trp Val Ile Phe Gly	Ala Tyr Ala Phe	Gly Ser
1498		50	55	60
1499	Cys Ile Asn His	Ser Met Thr Leu Ala	Ile His Glu Ile Ala	His
1500		65	70	75
1501	Asn Ala Ala Phe	Gly Asn Cys Lys Ala	Met Trp Asn Arg	Trp Phe
1502		80	85	90
1503	Gly Met Phe Ala	Asn Leu Pro Ile Gly	Ile Pro Tyr Ser Ile	Ser
1504		95	100	105
1505	Phe Lys Arg Tyr	His Met Asp His His	Arg Tyr Leu Gly Ala	Asp
1506		110	115	120
1507	Gly Val Asp Val	Asp Ile Pro Thr Asp	Phe Glu Gly Trp Phe	Phe
1508		125	130	135
1509	Cys Thr Ala Phe	Arg Lys Phe Ile Trp	Val Ile Leu Gln Pro	Leu
1510		140	145	150
1511	Phe Tyr Ala Phe	Arg Pro Leu Phe Ile	Asn Pro Lys Pro Ile	Thr
1512		155	160	165
1513	Tyr Leu Glu Val	Ile Asn Thr Val Ala	Gln Val Thr Phe Asp	Ile
1514		170	175	180
1515	Leu Ile Tyr Tyr	Phe Leu Gly Ile Lys	Ser Leu Val Tyr Met	Leu
1516		185	190	195
1517	Ala Ala Ser Leu	Leu Gly Leu Gly Leu	His Pro Ile Ser Gly	His
1518		200	205	210
1519	Phe Ile Ala Glu	His Tyr Met Phe Leu	Lys Gly His Glu Thr	Tyr
1520		215	220	225
1521	Ser Tyr Tyr Gly	Pro Leu Asn Leu Leu	Thr Phe Asn Val Gly	Tyr
1522		230	235	240
1523	His Asn Glu His	His Asp Phe Pro Asn	Ile Pro Gly Lys Ser	Leu
1524		245	250	255
1525	Pro Leu Val Arg	Lys Ile Ala Ala Glu	Tyr Tyr Asp Asn Leu	Pro
1526		260	265	270
1527	His Tyr Asn Ser	Trp Ile Lys Val Leu	Tyr Asp Phe Val Met	Asp
1528		275	280	285
1529	Asp Thr Ile Ser	Pro Tyr Ser Arg Met	Lys Arg His Gln Lys	Gly
1530		290	295	300
1531	Glu Met Val Leu	Glu Xaa Ile Ser Leu	Val Pro Lys Gly Phe	Phe
1532		305	310	315
1533	Ser Lys Thr Leu	Asp Asp Lys Met Glu	Phe Leu His Tyr Xaa	Thr
1534		320	325	330
1535	Xaa Asp Gln Xaa	Cys Ser Glu Ala Pro	Leu Ala Gln Phe Gln	Ser
1536		335	340	345
1537	Lys Ser Ser Val	Ile Pro Arg Ser Glu	Ser Gly Phe Xaa Thr	Val
1538		350	355	360
1539	Ser Leu Thr Leu	Tyr Cys Ser Val Ser	Leu Thr Gly Asn Leu	Xaa
1540		365	370	375
1541	Leu Val Tyr Tyr	Arg His Xaa Gly Cys	Phe Thr His Val Cys	His
1542		380	385	390
1543	Phe Ile Ser Ile	Ser Phe Lys Lys Leu	Lys Ser Tyr Phe Ala	
1544		400	405	410

395

400

405

INPUT SET: S35428.raw

1545 Arg  
1546

1593 (2) INFORMATION FOR SEQ ID NO:36:

1594

1595 (i) SEQUENCE CHARACTERISTICS:

--&gt; 1596 (A) LENGTH: 86 amino acids 87 shown

1597 (B) TYPE: amino acid

1598 (C) STRANDEDNESS: single

1599 (D) TOPOLOGY: linear

1600

1601 (ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

1602

1603 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

1604

1605

1606

1607 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala

1608 1 5 10 15

1609 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His

1610 20 25 30

1611 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His

1612 35 40 45

1613 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala

1614 50 55 60

1615 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn

1616 65 70 75

1617 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xaa

1618 80 85

1619

1620

1621

1679 (2) INFORMATION FOR SEQ ID NO:38:

1680

1681 (i) SEQUENCE CHARACTERISTICS:

--&gt; 1682 (A) LENGTH: 566 amino acids 562

1683 (B) TYPE: amino acid

1684 (C) STRANDEDNESS: single

1685 (D) TOPOLOGY: linear

1686

1687 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

1688

1689 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

1690

1691

1692 His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe

1693 1 5 10 15

1694 Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val

1695 20 25 30

1696 Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu

1697 35 40 45

1698 Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:40

INPUT SET: S35428.raw

1699				50					55				60		
1700	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr
1701				65					70						75
1702	Phe	Gln	Tyr	Gln	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp
1703				80					85						90
1704	Val	Asp	Leu	Ala	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile
1705				95					100						105
1706	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu
1707				110					115						120
1708	Asn	Phe	Ile	Arg	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr
1709				125					130						135
1710	Gln	Met	Asn	His	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg
1711				140					145						150
1712	Asp	Trp	Phe	Ser	Ser	Gln	Leu	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln
1713				155					160						165
1714	Ser	Phe	Phe	Asn	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile
1715				170					175						180
1716	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	His	Lys
1717				185					190						195
1718	Ile	Ala	Pro	Leu	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu
1719				200					205						210
1720	Tyr	Gln	Glu	Lys	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg
1721				215					220						225
1722	Ser	Leu	Lys	Lys	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His
1723				230					235						240
1724	Lys	Xaa	Ser	His	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg
1725				245					250						255
1726	Trp	Gly	Asp	Gly	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val
1727				260					265						270
1728	Ser	Glu	Arg	Leu	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp
1729				275					280						285
1730	Leu	Ser	Pro	Phe	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His
1731				290					295						300
1732	Ser	Thr	Leu	Pro	Ser	Trp	Asp	Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro
1733				305					310						315
1734	Ser	Ala	Met	Ala	Leu	Pro	Val	Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly
1735				320					325						330
1736	Ala	Glu	Arg	Trp	Pro	Pro	Gly	Val	Ala	Leu	Ser	Tyr	Leu	His	Ser
1737				335					340						345
1738	Leu	Pro	Leu	Lys	Met	Gly	Gly	Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala
1739				350					355						360
1740	Cys	Glu	Ser	Pro	Leu	Ala	Ala	Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala
1741				365					370						375
1742	Leu	Val	Leu	Gln	Met	Leu	Leu	Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser
1743				380					385						390
1744	Arg	Ala	Gly	Pro	Leu	Thr	Leu	Pro	Ala	Trp	Leu	His	Ser	Pro	Xaa
1745				400	395				405	400				410	405
1746	Arg	Leu	Pro	Leu	Val	His	Pro	Phe	Ile	Glu	Arg	Pro	Ala	Leu	Leu
1747				415					420						425
1748	Gln	Ser	Ser	Gly	Leu	Pro	Pro	Ala	Ala	Arg	Leu	Ser	Thr	Arg	Gly
1749				430					435						440
1750	Leu	Ser	Xaa	Asp	Val	Gln	Gly	Pro	Arg	Pro	Ala	Gly	Thr	Ala	Ser
1751				445					450						455

405  
numbering  
off



# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:40

INPUT SET: S35428.raw

1752 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser  
1753 460 465 470  
1754 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro  
1755 475 480 485  
1756 Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu  
1757 490 495 500  
1758 Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly  
1759 505 510 515  
1760 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val  
1761 520 525 530  
1762 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala  
1763 535 540 545  
1764 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala  
1765 550 555 560  
1766 Pro Gly Asp Val Gly Pro Xaa  
1767 565  
1768  
1769

numbering  
off  
↓

1770 (2) INFORMATION FOR SEQ ID NO:39:

1771

(i) SEQUENCE CHARACTERISTICS:

--> 1773 (A) LENGTH: 619 amino acids 6/5

1774 (B) TYPE: amino acid

1775 (C) STRANDEDNESS: single

1776 (D) TOPOLOGY: linear

1777

1778 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

1779

1780 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

1781

1782

1783

1784 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala

1785 1 5 10 15

1786 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His

1787 20 25 30

1788 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His

1789 35 40 45

1790 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala

1791 50 55 60

1792 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn

1793 65 70 75

1794 Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val

1795 80 85 90

1796 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys

1797 95 100 105

1798 Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly

1799 110 115 120

1800 Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met

1801 125 130 135

1802 Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val

1803 140 145 150

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:41

INPUT SET: S35428.raw

1804	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly
1805					155					160					165
1806	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	Phe	Leu	Glu
1807					170					175					180
1808	Ser	His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Val	Met
1809					185					190					195
1810	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	Ser	Gln	Leu
1811					200					205					210
1812	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	Asp	Trp	Phe
1813					215					220					225
1814	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr
1815					230					235					240
1816	Met	Pro	Arg	His	Asn	Leu	His	Lys	Ile	Ala	Pro	Leu	Val	Lys	Ser
1817					245					250					255
1818	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Glu	Lys	Pro	Leu	Leu
1819					260					265					270
1820	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	Ser	Leu	Lys	Lys	Ser	Gly	Lys
1821					275					280					285
1822	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Lys	Xaa	Ser	His	Ser	Pro	Arg
1823					290					295					300
1824	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp	Gly	Asp	Gly	Gln	Arg	Asn
1825					305					310					315
1826	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val	Ser	Glu	Arg	Leu	Val	Tyr	Ala
1827					320					325					330
1828	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro	Phe	Leu	Leu	Ser
1829					335					340					345
1830	Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro	Ser	Trp	Asp
1831					350					355					360
1832	Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	Ser	Ala	Met	Ala	Leu	Pro	Val
1833					365					370					375
1834	Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	Ala	Glu	Arg	Trp	Pro	Pro	Gly
1835					380					385					390
1836	Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	Leu	Pro	Leu	Lys	Met	Gly	Gly
1837					400	395				405	400			410	405
1838	Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	Cys	Glu	Ser	Pro	Leu	Ala	Ala
1839					415					420					425
1840	Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	Leu	Val	Leu	Gln	Met	Leu	Leu
1841					430					435					440
1842	Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	Arg	Ala	Gly	Pro	Leu	Thr	Leu
1843					445					450					455
1844	Pro	Ala	Trp	Leu	His	Ser	Pro	Xaa	Arg	Leu	Pro	Leu	Val	His	Pro
1845					460					465					470
1846	Phe	Ile	Glu	Arg	Pro	Ala	Leu	Leu	Gln	Ser	Ser	Gly	Leu	Pro	Pro
1847					475					480					485
1848	Ala	Ala	Arg	Leu	Ser	Thr	Arg	Gly	Leu	Ser	Xaa	Asp	Val	Gln	Gly
1849					490					495					500
1850	Pro	Arg	Pro	Ala	Gly	Thr	Ala	Ser	Pro	Asn	Leu	Gly	Pro	Trp	Lys
1851					505					510					515
1852	Ser	Pro	Pro	Pro	His	His	Xaa	Ser	Ala	Leu	Thr	Leu	Gly	Phe	His
1853					520					525					530
1854	Gly	Pro	His	Ser	Thr	Ala	Ser	Pro	Thr	Xaa	Ala	Cys	Asp	Leu	Gly
1855					535					540					545
1856	Thr	Lys	Gly	Gly	Val	Pro	Arg	Leu	Leu	Xaa	Leu	Ser	Arg	Gly	Ser

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:41

INPUT SET: S35428.raw

1857		550		555		560
1858	Gly His Val Gln	Gly Gly Ala Gly Trp	Pro Gly Gly Ser Ala His			
1859		565		570		575
1860	Pro Pro Ala Phe	Pro Gln Gly Val Leu	Arg Ser Lys Ile Leu Glu			
1861		580		585		590
1862	Gln Ser Asp Pro	Ser Pro Lys Ala Leu	Leu Ser Ala Gly Gln Cys			
1863		595		600		605
1864	Gln Pro Ile Pro	Gly His Leu Ala Pro	Gly Asp Val Gly Pro Xaa			
1865		610		615		620
1866						
1867						
1868						

renewing

↓

1869 (2) INFORMATION FOR SEQ ID NO:40:

1870

1871 (i) SEQUENCE CHARACTERISTICS:

--> 1872 (A) LENGTH: 757 amino acids

1873 (B) TYPE: amino acid

1874 (C) STRANDEDNESS: single

1875 (D) TOPOLOGY: linear

1876

1877 (ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

1878

1879 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

1880

1881

1882 Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln

1883 1 5 10 15

1884 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val

1885 20 25 30

1886 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg

1887 35 40 45

1888 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val

1889 50 55 60

1890 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser

1891 65 70 75

1892 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro

1893 80 85 90

1894 Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala

1895 95 100 105

1896 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe

1897 110 115 120

1898 Leu Leu Tyr Leu Leu His Ile Leu Leu Asp Gly Ala Ala Trp

1899 125 130 135

1900 Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu

1901 140 145 150

1902 Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp

1903 155 160 165

1904 Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys

1905 170 175 180

1906 Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly

1907 185 190 195

1908 Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala

753

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/367,013

DATE: 05/05/2000  
TIME: 11:03:42

INPUT SET: S35428.raw

1909		200		205		210
1910	Lys Pro Asn Ile	Phe His Lys Asp Pro	Asp Val Asn Met Leu	His		
1911		215		220		225
1912	Val Phe Val Leu	Gly Glu Trp Gln Pro	Ile Glu Tyr Gly Lys	Lys		
1913		230		235		240
1914	Lys Leu Lys Tyr	Leu Pro Tyr Asn His	Gln His Glu Tyr Phe	Phe		
1915		245		250		255
1916	Leu Ile Gly Pro	Pro Leu Leu Ile Pro	Met Tyr Phe Gln Tyr	Gln		
1917		260		265		270
1918	Ile Ile Met Thr	Met Ile Val His Lys	Asn Trp Val Asp Leu	Ala		
1919		275		280		285
1920	Trp Ala Val Ser	Tyr Tyr Ile Arg Phe	Phe Ile Thr Tyr Ile	Pro		
1921		290		295		300
1922	Phe Tyr Gly Ile	Leu Gly Ala Leu Leu	Phe Leu Asn Phe Ile	Arg		
1923		305		310		315
1924	Phe Leu Glu Ser	His Trp Phe Val Trp	Val Thr Gln Met Asn	His		
1925		320		325		330
1926	Ile Val Met Glu	Ile Asp Gln Glu Ala	Tyr Arg Asp Trp Phe	Ser		
1927		335		340		345
1928	Ser Gln Leu Thr	Ala Thr Cys Asn Val	Glu Gln Ser Phe Phe	Asn		
1929		350		355		360
1930	Asp Trp Phe Ser	Gly His Leu Asn Phe	Gln Ile Glu His His	Leu		
1931		365		370		375
1932	Phe Pro Thr Met	Pro Arg His Asn Leu	His Lys Ile Ala Pro	Leu		
1933		380		385		390
1934	Val Lys Ser Leu	Cys Ala Lys His Gly	Ile Glu Tyr Gln Glu	Lys		
1935		400		405		410
1936	Pro Leu Leu Arg	Ala Leu Leu Asp Ile	Ile Arg Ser Leu Lys	Lys		
1937		415		420		425
1938	Ser Gly Lys Leu	Trp Leu Asp Ala Tyr	Leu His Lys Xaa Ser	His		
1939		430		435		440
1940	Ser Pro Arg Asp	Thr Val Gly Lys Gly	Cys Arg Trp Gly Asp	Gly		
1941		445		450		455
1942	Gln Arg Asn Asp	Gly Leu Leu Phe Xaa	Gly Val Ser Glu Arg	Leu		
1943		460		465		470
1944	Val Tyr Ala Leu	Leu Thr Asp Pro Met	Leu Asp Leu Ser Pro	Phe		
1945		475		480		485
1946	Leu Leu Ser Phe	Phe Ser Ser His Leu	Pro His Ser Thr Leu	Pro		
1947		490		495		500
1948	Ser Trp Asp Leu	Pro Ser Leu Ser Arg	Gln Pro Ser Ala Met	Ala		
1949		505		510		515
1950	Leu Pro Val Pro	Pro Ser Pro Phe Phe	Gln Gly Ala Glu Arg	Trp		
1951		520		525		530
1952	Pro Pro Gly Val	Ala Leu Ser Tyr Leu	His Ser Leu Pro Leu	Lys		
1953		535		540		545
1954	Met Gly Gly Asp	Gln Arg Ser Met Gly	Leu Ala Cys Glu Ser	Pro		
1955		550		555		560
1956	Leu Ala Ala Trp	Ser Leu Gly Ile Thr	Pro Ala Leu Val Leu	Gln		
1957		565		570		575
1958	Met Leu Leu Gly	Phe Ile Gly Ala Gly	Pro Ser Arg Ala Gly	Pro		
1959		580		585		590
1960	Leu Thr Leu Pro	Ala Trp Leu His Ser	Pro Xaa Arg Leu Pro	Leu		
1961		595		600		605

405 400 410 405 numbering  
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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/367,013DATE: 05/05/2000  
TIME: 11:03:42

INPUT SET: S35428.raw

1962	Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly	610	615	620
1963		610	615	620
1964	Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser Xaa Asp	625	630	635
1965		625	630	635
1966	Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly	640	645	650
1967		640	645	650
1968	Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser Ala Leu Thr Leu	655	660	665
1969		655	660	665
1970	Gly Phe His Gly Pro His Ser Thr Ala Ser Pro Thr Xaa Ala Cys	670	675	680
1971		670	675	680
1972	Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa Leu Ser	685	690	695
1973		685	690	695
1974	Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly	700	705	710
1975		700	705	710
1976	Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys	715	720	725
1977		715	720	725
1978	Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala	730	735	740
1979		730	735	740
1980	Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val	745	750	755
1981		745	750	755
1982	Gly Pro Xaa			
1983				
1984				
1985				
1986	-143-			
1987				
1988	SUBSTITUTE SHEET			
1989				
1990				

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SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/09/367,013DATE: 05/05/2000  
TIME: 11:03:42

INPUT SET: S35428.raw

Line	Error	Original Text
33	Unknown or Misplaced Identifier	(B) (B) FILING DATE:
860	Entered (227) and Calc. Seq. Length (228) differ	(A) LENGTH: 227 amino acids
930	Entered (87) and Calc. Seq. Length (102) differ	(A) LENGTH: 87 amino acids
962	Entered (520) and Calc. Seq. Length (0) differ	(A) LENGTH: 520 nucleic acids
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
972	Wrong Amino Acid Designator	GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCG
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
973	Wrong Amino Acid Designator	CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA
974	Wrong Amino Acid Designator	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACC
974	Wrong Amino Acid Designator	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACC
974	Wrong Amino Acid Designator	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACC
974	Wrong Amino Acid Designator	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACC
974	Wrong Amino Acid Designator	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACC
974	Wrong Amino Acid Designator	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACC
975	Wrong Amino Acid Designator	GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCAC
975	Wrong Amino Acid Designator	GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCAC
975	Wrong Amino Acid Designator	GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCAC
975	Wrong Amino Acid Designator	GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCAC
975	Wrong Amino Acid Designator	GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCAC
975	Wrong Amino Acid Designator	GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCAC
976	Wrong Amino Acid Designator	GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTT
976	Wrong Amino Acid Designator	GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTT
976	Wrong Amino Acid Designator	GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTT
976	Wrong Amino Acid Designator	GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTT
976	Wrong Amino Acid Designator	GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTT
976	Wrong Amino Acid Designator	GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTT
977	Wrong Amino Acid Designator	CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCG
977	Wrong Amino Acid Designator	CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCG
977	Wrong Amino Acid Designator	CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCG
977	Wrong Amino Acid Designator	CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCG
977	Wrong Amino Acid Designator	CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCG
977	Wrong Amino Acid Designator	CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCG
978	Wrong Amino Acid Designator	ACGGTCTCCC TTACTIONGAC ATGCCCTACA CGAGC
978	Wrong Amino Acid Designator	ACGGTCTCCC TTACTIONGAC ATGCCCTACA CGAGC
978	Wrong Amino Acid Designator	ACGGTCTCCC TTACTIONGAC ATGCCCTACA CGAGC
978	Wrong Amino Acid Designator	ACGGTCTCCC TTACTIONGAC ATGCCCTACA CGAGC
978	Wrong Amino Acid Designator	ACGGTCTCCC TTACTIONGAC ATGCCCTACA CGAGC
978	Wrong Amino Acid Designator	ACGGTCTCCC TTACTIONGAC ATGCCCTACA CGAGC
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/367,013**DATE: 05/05/2000  
TIME: 11:03:42**INPUT SET: S35428.raw**

Line	Error	Original Text
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
979	Wrong Amino Acid Designator	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAG
980	Wrong Amino Acid Designator	TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTC
980	Wrong Amino Acid Designator	TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTC
980	Wrong Amino Acid Designator	TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTC
980	Wrong Amino Acid Designator	TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTC
1046	Entered (125) and Calc. Seq. Length (140) differ	(A) LENGTH: 125 amino acids
1481	Entered (411) and Calc. Seq. Length (406) differ	(A) LENGTH: 411 amino acids
1596	Entered (86) and Calc. Seq. Length (87) differ	(A) LENGTH: 86 amino acids
1682	Entered (566) and Calc. Seq. Length (562) differ	(A) LENGTH: 566 amino acids
1773	Entered (619) and Calc. Seq. Length (615) differ	(A) LENGTH: 619 amino acids
1872	Entered (757) and Calc. Seq. Length (753) differ	(A) LENGTH: 757 amino acids
1988	Wrong Amino Acid Designator	SUBSTITUTE SHEET
1988	Wrong Amino Acid Designator	SUBSTITUTE SHEET